

Sayegh, Mohamed

<120> A Gene Encoding a Multidrug Resistance Human P-Glycoprotein  
Homologue on Chromosome 7p15-21 and Uses Thereof

<130> 81994/268611

<160> 19

<170> PatentIn version 3.0

<210> 1

<211> 659

<212> PRT

<213> Homo sapiens

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Gln Met Glu Ser Met Thr Tyr Ser Thr Glu Arg Lys Thr Asn Ser Leu  
35 40 45

Pro Leu His Ser Val Lys Ser Ile Lys Ser Asp Phe Ile Asp Lys Ala  
50 55 60

Glu Glu Ser Thr Gln Ser Lys Glu Ile Ser Leu Pro Glu Val Ser Leu  
65 70 75 80

Leu Lys Ile Leu Lys Leu Asn Lys Pro Glu Trp Pro Phe Val Val Leu  
85 90 95

Gly Thr Leu Ala Ser Val Leu Asn Gly Thr Val His Pro Val Phe Ser  
100 105 110

Ile Ile Phe Ala Lys Ile Ile Thr Met Phe Gly Asn Asn Asp Lys Thr  
115 120 125

Thr Leu Lys His Asp Ala Glu Ile Tyr Ser Met Ile Phe Val Ile Leu  
130 135 140

Gly Val Ile Cys Phe Val Ser Tyr Phe Met Gln Gly Leu Phe Tyr Gly  
145 150 155 160

[illegible]

Arg	Ala	Gly	Glu	Ile	Leu	Thr	Met	Arg	Leu	Arg	His	Leu	Ala	Phe	Lys	
				165					170					175		
Ala	Met	Leu	Tyr	Gln	Asp	Ile	Ala	Trp	Phe	Asp	Glu	Lys	Glu	Asn	Ser	
				180					185					190		
Thr	Gly	Gly	Leu	Thr	Thr	Ile	Leu	Ala	Ile	Asp	Ile	Ala	Gln	Ile	Gln	
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Gly	Ala	Thr	Gly	Ser	Arg	Ile	Gly	Val	Leu	Thr	Gln	Asn	Ala	Thr	Asn	
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Met	Gly	Leu	Ser	Val	Ile	Ile	Ser	Phe	Ile	Tyr	Gly	Trp	Glu	Met	Thr	
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Phe	Leu	Ile	Leu	Ser	Ile	Ala	Pro	Val	Leu	Ala	Val	Thr	Gly	Met	Ile	
				245					250					255		
Glu	Thr	Ala	Ala	Met	Thr	Gly	Phe	Ala	Asn	Lys	Asp	Lys	Gln	Glu	Leu	
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Lys	His	Ala	Gly	Lys	Ile	Ala	Thr	Glu	Ala	Leu	Glu	Asn	Ile	Arg	Thr	
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Ile	Val	Ser	Leu	Thr	Arg	Glu	Lys	Ala	Phe	Glu	Gln	Met	Tyr	Glu	Glu	
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Met	Leu	Gln	Thr	Gln	His	Arg	Asn	Thr	Ser	Lys	Lys	Ala	Gln	Ile	Ile	
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Gly	Ser	Cys	Tyr	Ala	Phe	Ser	His	Ala	Phe	Ile	Tyr	Phe	Ala	Tyr	Ala	
				325					330					335		
Ala	Gly	Phe	Arg	Phe	Gly	Ala	Tyr	Leu	Ile	Gln	Ala	Gly	Arg	Met	Thr	
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Pro	Glu	Gly	Met	Phe	Ile	Val	Phe	Thr	Ala	Ile	Ala	Tyr	Gly	Ala	Met	
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Ala	Ile	Gly	Lys	Thr	Leu	Val	Leu	Ala	Pro	Glu	Tyr	Ser	Lys	Ala	Lys	
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Ser	Gly	Ala	Ala	His	Leu	Phe	Ala	Leu	Leu	Glu	Lys	Lys	Pro	Asn	Ile	
				385					390					395		
Asp	Ser	Arg	Ser	Gln	Glu	Gly	Lys	Lys	Pro	Asp	Thr	Cys	Glu	Gly	Asn	
				405					410					415		
Leu	Glu	Phe	Arg	Glu	Val	Ser	Phe	Phe	Tyr	Pro	Cys	Arg	Pro	Asp	Val	
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Phe	Ile	Leu	Arg	Gly	Leu	Ser	Leu	Ser	Ile	Glu	Arg	Gly	Lys	Thr	Val	
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				465					470					475		
Val	Asp	Ala	Lys	Glu	Leu	Asn	Val	Gln	Trp	Leu	Arg	Ser	Gln	Ile	Ala	
				485					490					495		

Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg  
85 90 95

Asn Pro Lys Ile Leu Ile Leu Asp Glu Ala Thr Ser Ala Leu Asp Ser  
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 Glu Ser Lys Ser Ala Val Gln Ala Ala Leu Glu Lys Ala Ser Lys Gly  
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 Arg Thr Thr Ile Val Val Ala His Arg Leu Ser Thr Ile Arg Ser Ala  
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 Asp Leu Ile Val Thr Leu Lys Asp Gly Met Leu Ala Glu Lys Gly Ala  
 145 150 155 160  
 His Ala Glu Leu Met Ala Lys Arg Gly Leu Tyr Tyr Ser Leu Val Met  
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 Ser Gln Asp Ile Lys Lys Ala Asp Glu Gln Met Glu Ser Met Thr Tyr  
 180 185 190  
 Ser Thr Glu Arg Lys Thr Asn Ser Leu Pro Leu His Ser Val Lys Ser  
 195 200 205  
 Ile Lys Ser Asp Phe Ile Asp Lys Ala Glu Glu Ser Thr Gln Ser Lys  
 210 215 220  
 Glu Ile Ser Leu Pro Glu Val Ser Leu Leu Lys Ile Leu Lys Leu Asn  
 225 230 235 240  
 Lys Pro Glu Trp Pro Phe Val Val Leu Gly Thr Leu Ala Ser Val Leu  
 245 250 255  
 Asn Gly Thr Val His Pro Val Phe Ser Ile Ile Phe Ala Lys Ile Ile  
 260 265 270  
 Thr Met Phe Gly Asn Asn Asp Lys Thr Thr Leu Lys His Asp Ala Glu  
 275 280 285  
 Ile Tyr Ser Met Ile Phe Val Ile Leu Gly Val Ile Cys Phe Val Ser  
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 Tyr Phe Met Gln Gly Leu Phe Tyr Gly Arg Ala Gly Glu Ile Leu Thr  
 305 310 315 320  
 Met Arg Leu Arg His Leu Ala Phe Lys Ala Met Leu Tyr Gln Asp Ile  
 325 330 335  
 Ala Trp Phe Asp Glu Lys Glu Asn Ser Thr Gly Gly Leu Thr Thr Ile  
 340 345 350  
 Leu Ala Ile Asp Ile Ala Gln Ile Gln Gly Ala Thr Gly Ser Arg Ile  
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 Gly Val Leu Thr Gln Asn Ala Thr Asn Met Gly Leu Ser Val Ile Ile  
 370 375 380  
 Ser Phe Ile Tyr Gly Trp Glu Met Thr Phe Leu Ile Leu Ser Ile Ala  
 385 390 395 400  
 Pro Val Leu Ala Val Thr Gly Met Ile Glu Thr Ala Ala Met Thr Gly  
 405 410 415  
 Phe Ala Asn Lys Asp Lys Gln Glu Leu Lys His Ala Gly Lys Ile Ala  
 420 425 430

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Lys	Ala	Phe	Glu	Gln	Met	Tyr	Glu	Glu	Met	Leu	Gln	Thr	Gln	His	Arg
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Asn	Thr	Ser	Lys	Lys	Ala	Gln	Ile	Ile	Gly	Ser	Cys	Tyr	Ala	Phe	Ser
465					470					475					480
His	Ala	Phe	Ile	Tyr	Phe	Ala	Tyr	Ala	Ala	Gly	Phe	Arg	Phe	Gly	Ala
				485					490					495	
Tyr	Leu	Ile	Gln	Ala	Gly	Arg	Met	Thr	Pro	Glu	Gly	Met	Phe	Ile	Val
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Phe	Thr	Ala	Ile	Ala	Tyr	Gly	Ala	Met	Ala	Ile	Gly	Lys	Thr	Leu	Val
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Lys	Lys	Pro	Asp	Thr	Cys	Glu	Gly	Asn	Leu	Glu	Phe	Arg	Glu	Val	Ser
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Leu	Ser	Ile	Glu	Arg	Gly	Lys	Thr	Val	Ala	Phe	Val	Gly	Ser	Ser	Gly
		595					600					605			
Cys	Gly	Lys	Ser	Thr	Ser	Val	Gln	Leu	Leu	Gln	Arg	Leu	Tyr	Asp	Pro
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Val	Gln	Trp	Leu	Arg	Ser	Gln	Ile	Ala	Ile	Val	Pro	Gln	Glu	Pro	Val
				645					650					655	
Leu	Phe	Asn	Cys	Ser	Ile	Ala	Glu	Asn	Ile	Ala	Tyr	Gly	Asp	Asn	Ser
			660					665					670		
Arg	Val	Val	Pro	Leu	Asp	Glu	Ile	Lys	Glu	Ala	Ala	Asn	Ala	Ala	Asn
		675					680					685			
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705					710					715					720
Ile	Ala	Arg	Ala	Leu	Leu	Gln	Lys	Pro	Lys	Ile	Leu	Leu	Leu	Asp	Glu
				725					730					735	
Ala	Thr	Ser	Ala	Leu	Asp	Asn	Asp	Ser	Glu	Lys	Val	Val	Gln	His	Ala
			740					745					750		
Leu	Asp	Lys	Ala	Arg	Thr	Gly	Arg	Thr	Cys	Leu	Val	Val	Thr	His	Arg
		755					760					765			

Leu Ser Ala Ile Gln Asn Ala Asp Leu Ile Val Val Leu His Asn Gly  
770 775 780

Lys Ile Lys Glu Gln Gly Thr His Gln Glu Leu Leu Arg Asn Arg Asp  
785 790 795 800

Ile Tyr Phe Lys Leu Val Asn Ala Gln Ser Val Gln  
805 810

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<211> 131

<212> PRT

<213> Homo sapiens

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Ile Ser Asn Asn Ile Lys Tyr Gly Arg Asp Asp Val Thr Asp Glu Glu  
35 40 45

Met Glu Arg Ala Ala Arg Glu Ala Asn Ala Tyr Asp Phe Ile Met Glu  
50 55 60

Phe Pro Asn Lys Phe Asn Thr Leu Val Gly Glu Lys Gly Ala Gln Met  
65 70 75 80

Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg  
85 90 95

Asn Pro Lys Ile Leu Ile Leu Asp Glu Ala Thr Ser Ala Leu Asp Ser  
100 105 110

Glu Ser Lys Ser Ala Val Gln Ala Ala Leu Glu Lys Asp Thr Pro Arg  
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Tyr Ser Phe  
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<211> 1058

<212> PRT

<213> Homo sapiens

<220>

<221> Note

<222> (66)..(66)

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Phe	Arg	Ala 35	Gln	Glu	Lys	Glu	Leu 40	Gln	Arg	Ser	Phe	Leu 45	Leu	Asn	Ile
Thr	Arg 50	Tyr	Ala	Trp	Phe	Tyr 55	Phe	Pro	Gln	Trp	Leu 60	Leu	Ser	Cys	Val
Leu 65	Xaa	Phe	Val	Arg	Tyr 70	Thr	Gln	Asn	Leu	Lys 75	Asp	Ala	Lys	Asp	Phe 80
Gly	Ile	Lys	Arg	Thr 85	Ile	Ala	Ser	Lys 90	Val	Ser	Leu	Gly	Ala 95	Val	Tyr
Phe	Phe	Met	Asn 100	Gly	Thr	Tyr	Gly	Leu 105	Ala	Phe	Trp	Tyr	Gly 110	Thr	Ser
Leu	Ile	Leu 115	Asn	Gly	Glu	Pro	Gly 120	Tyr	Thr	Ile	Gly	Thr 125	Val	Leu	Ala
Val	Phe 130	Phe	Ser	Val	Ile	His 135	Ser	Ser	Tyr	Cys	Ile 140	Gly	Ala	Ala	Val
Pro 145	His	Phe	Glu	Thr	Phe 150	Ala	Ile	Ala	Arg	Gly 155	Ala	Ala	Phe	His	Ile 160
Phe	Gln	Val	Ile	Asp 165	Lys	Lys	Pro	Ser	Ile 170	Asp	Asn	Phe	Ser	Thr 175	Ala
Gly	Tyr	Lys	Pro 180	Glu	Ser	Ile	Glu	Gly 185	Thr	Val	Glu	Phe	Lys 190	Asn	Val
Ser	Phe	Asn 195	Tyr	Pro	Ser	Arg	Pro 200	Ser	Ile	Lys	Ile	Leu 205	Lys	Gly	Leu
Asn	Leu 210	Arg	Ile	Lys	Ser	Gly 215	Glu	Thr	Val	Ala	Leu 220	Val	Gly	Leu	Asn
Gly 225	Ser	Gly	Lys	Ser	Thr 230	Val	Val	Gln	Leu	Leu 235	Gln	Arg	Leu	Tyr	Asp 240
Pro	Asp	Asp	Gly	Phe 245	Ile	Met	Val	Asp	Glu 250	Asn	Asp	Ile	Arg	Ala 255	Leu
Asn	Val	Arg	His 260	Tyr	Arg	Asp	His 265	Ile	Gly	Val	Val	Ser	Gln 270	Glu	Pro
Val	Leu	Phe 275	Gly	Thr	Thr	Ile	Ser 280	Asn	Asn	Ile	Lys	Tyr 285	Gly	Arg	Asp
Asp	Val 290	Thr	Asp	Glu	Glu	Met 295	Glu	Arg	Ala	Ala	Arg 300	Glu	Ala	Asn	Ala

Tyr Asp Phe Ile Met Glu Phe Pro Asn Lys Phe Asn Thr Leu Val Gly  
 305 310 315 320  
 Glu Lys Gly Ala Gln Met Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile  
 325 330 335  
 Ala Arg Ala Leu Val Arg Asn Pro Lys Ile Leu Ile Leu Asp Glu Ala  
 340 345 350  
 Thr Ser Ala Leu Asp Ser Glu Ser Lys Ser Ala Val Gln Ala Ala Leu  
 355 360 365  
 Glu Lys Ala Ser Lys Gly Arg Thr Thr Ile Val Val Ala His Arg Leu  
 370 375 380  
 Ser Thr Ile Arg Ser Ala Asp Leu Ile Val Thr Leu Lys Asp Gly Met  
 385 390 395 400  
 Leu Ala Glu Lys Gly Ala His Ala Glu Leu Met Ala Lys Arg Gly Leu  
 405 410 415  
 Tyr Tyr Ser Leu Val Met Ser Gln Asp Ile Lys Lys Ala Asp Glu Gln  
 420 425 430  
 Met Glu Ser Met Thr Tyr Ser Thr Glu Arg Lys Thr Asn Ser Leu Pro  
 435 440 445  
 Leu His Ser Val Lys Ser Ile Lys Ser Asp Phe Ile Asp Lys Ala Glu  
 450 455 460  
 Glu Ser Thr Gln Ser Lys Glu Ile Ser Leu Pro Glu Val Ser Leu Leu  
 465 470 475 480  
 Lys Ile Leu Lys Leu Asn Lys Pro Glu Trp Pro Phe Val Val Leu Gly  
 485 490 495  
 Thr Leu Ala Ser Val Leu Asn Gly Thr Val His Pro Val Phe Ser Ile  
 500 505 510  
 Ile Phe Ala Lys Ile Ile Thr Met Phe Gly Asn Asn Asp Lys Thr Thr  
 515 520 525  
 Leu Lys His Asp Ala Glu Ile Tyr Ser Met Ile Phe Val Ile Leu Gly  
 530 535 540  
 Val Ile Cys Phe Val Ser Tyr Phe Met Gln Gly Leu Phe Tyr Gly Arg  
 545 550 555 560  
 Ala Gly Glu Ile Leu Thr Met Arg Leu Arg His Leu Ala Phe Lys Ala  
 565 570 575  
 Met Leu Tyr Gln Asp Ile Ala Trp Phe Asp Glu Lys Glu Asn Ser Thr  
 580 585 590  
 Gly Gly Leu Thr Thr Ile Leu Ala Ile Asp Ile Ala Gln Ile Gln Gly  
 595 600 605  
 Ala Thr Gly Ser Arg Ile Gly Val Leu Thr Gln Asn Ala Thr Asn Met  
 610 615 620  
 Gly Leu Ser Val Ile Ile Ser Phe Ile Tyr Gly Trp Glu Met Thr Phe  
 625 630 635 640

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Leu 642	Ile 643	Leu 644	Ser 645	Ile 646	Ala 647	Pro 648	Val 649	Leu 650	Ala 651	Val 652	Thr 653	Gly 654	Met 655	Ile 656	Glu 657
Thr 658	Ala 659	Ala 660	Met 661	Thr 662	Gly 663	Phe 664	Ala 665	Asn 666	Lys 667	Asp 668	Lys 669	Gln 670	Glu 671	Leu 672	Lys 673
His 674	Ala 675	Gly 676	Lys 677	Ile 678	Ala 679	Thr 680	Glu 681	Ala 682	Leu 683	Glu 684	Asn 685	Ile 686	Arg 687	Thr 688	Ile 689
Val 690	Ser 691	Leu 692	Thr 693	Arg 694	Glu 695	Lys 696	Ala 697	Phe 698	Glu 699	Gln 700	Met 701	Tyr 702	Glu 703	Glu 704	Met 705
Leu 706	Gln 707	Thr 708	Gln 709	His 710	Arg 711	Asn 712	Thr 713	Ser 714	Lys 715	Lys 716	Ala 717	Gln 718	Ile 719	Ile 720	Gly 721
Ser 722	Cys 723	Tyr 724	Ala 725	Phe 726	Ser 727	His 728	Ala 729	Phe 730	Ile 731	Tyr 732	Phe 733	Ala 734	Tyr 735	Ala 736	Ala 737
Gly 738	Phe 739	Arg 740	Phe 741	Gly 742	Ala 743	Tyr 744	Leu 745	Ile 746	Gln 747	Ala 748	Gly 749	Arg 750	Met 751	Thr 752	Pro 753
Glu 754	Gly 755	Met 756	Phe 757	Ile 758	Val 759	Phe 760	Thr 761	Ala 762	Ile 763	Ala 764	Tyr 765	Gly 766	Ala 767	Met 768	Ala 769
Ile 770	Gly 771	Lys 772	Thr 773	Leu 774	Val 775	Leu 776	Ala 777	Pro 778	Glu 779	Tyr 780	Ser 781	Lys 782	Ala 783	Lys 784	Ser 785
Gly 786	Ala 787	Ala 788	His 789	Leu 790	Phe 791	Ala 792	Leu 793	Leu 794	Glu 795	Lys 796	Lys 797	Pro 798	Asn 799	Ile 800	Asp 801
Ser 802	Arg 803	Ser 804	Gln 805	Glu 806	Gly 807	Lys 808	Lys 809	Pro 810	Asp 811	Thr 812	Cys 813	Glu 814	Gly 815	Asn 816	Leu 817
Glu 818	Phe 819	Arg 820	Glu 821	Val 822	Ser 823	Phe 824	Phe 825	Tyr 826	Pro 827	Cys 828	Arg 829	Pro 830	Asp 831	Val 832	Phe 833
Ile 834	Leu 835	Arg 836	Gly 837	Leu 838	Ser 839	Leu 840	Ser 841	Ile 842	Glu 843	Arg 844	Gly 845	Lys 846	Thr 847	Val 848	Ala 849
Phe 850	Val 851	Gly 852	Ser 853	Ser 854	Gly 855	Cys 856	Gly 857	Lys 858	Ser 859	Thr 860	Ser 861	Val 862	Gln 863	Leu 864	Leu 865
Gln 866	Arg 867	Leu 868	Tyr 869	Asp 870	Pro 871	Val 872	Gln 873	Gly 874	Gln 875	Val 876	Leu 877	Phe 878	Asp 879	Gly 880	Val 881
Asp 882	Ala 883	Lys 884	Glu 885	Leu 886	Asn 887	Val 888	Gln 889	Trp 890	Leu 891	Arg 892	Ser 893	Gln 894	Ile 895	Ala 896	Ile 897
Val 898	Pro 899	Gln 900	Glu 901	Pro 902	Val 903	Leu 904	Phe 905	Asn 906	Cys 907	Ser 908	Ile 909	Ala 910	Glu 911	Asn 912	Ile 913
Ala 914	Tyr 915	Gly 916	Asp 917	Asn 918	Ser 919	Arg 920	Val 921	Val 922	Pro 923	Leu 924	Asp 925	Glu 926	Ile 927	Lys 928	Glu 929
Ala 930	Ala 931	Asn 932	Ala 933	Ala 934	Asn 935	Ile 936	His 937	Ser 938	Phe 939	Ile 940	Glu 941	Gly 942	Leu 943	Pro 944	Glu 945
Lys 946	Tyr 947	Asn 948	Thr 949	Gln 950	Val 951	Gly 952	Leu 953	Lys 954	Gly 955	Ala 956	Gln 957	Leu 958	Ser 959	Gly 960	Gly 961
Gln 962	Lys 963	Gln 964	Arg 965	Leu 966	Ala 967	Ile 968	Ala 969	Arg 970	Ala 971	Leu 972	Leu 973	Gln 974	Lys 975	Pro 976	Lys 977

Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Asn Asp Ser Glu  
                   980                  985                  990

Lys Val Val Gln His Ala Leu Asp Lys Ala Arg Thr Gly Arg Thr Cys  
                   995                  1000                  1005

Leu Val Val Thr His Arg Leu Ser Ala Ile Gln Asn Ala Asp Leu  
                   1010                  1015                  1020

Ile Val Val Leu His Asn Gly Lys Ile Lys Glu Gln Gly Thr His  
                   1025                  1030                  1035

Gln Glu Leu Leu Arg Asn Arg Asp Ile Tyr Phe Lys Leu Val Asn  
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Ala Gln Ser Val Gln  
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<210> 5

<211> 1222

<212> PRT

<213> Homo sapiens

<220>

<221> Note

<222> (230)..(230)

<223> Xaa at position 230 represents any L amino acid

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Cys Leu Val Gln Thr Asn Thr Tyr Ser Phe Phe Arg Leu Thr Leu Tyr  
                   35                  40                  45

Tyr Val Gly Ile Gly Val Ala Ala Leu Ile Phe Gly Tyr Ile Gln Ile  
                   50                  55                  60

Ser Leu Trp Ile Ile Thr Ala Ala Arg Gln Thr Lys Arg Ile Arg Lys  
   65                  70                  75                  80

Gln Phe Phe His Ser Val Leu Ala Gln Asp Ile Gly Trp Phe Asp Ser  
                   85                  90                  95

Cys Asp Ile Gly Glu Leu Asn Thr Arg Met Thr Asp Ile Asp Lys Ile  
                   100                  105                  110

Ser Asp Gly Ile Gly Asp Lys Ile Ala Leu Leu Phe Gln Asn Met Ser  
                   115                  120                  125

1234567891011121314151617181920212223242526272829303132333435363738394041424344454647484950515253545556575859606162636465666768697071727374757677787980818283848586878889909192939495969798991001011021031041051061071081091101111121131141151161171181191201211221231241251261271281291301311321331341351361371381391401411421431441451461471481491501511521531541551561571581591601611621631641651661671681691701711721731741751761771781791801811821831841851861871881891901911921931941951961971981992002012022032042052062072082092102112122132142152162172182192202212222232242252262272282292302312322332342352362372382392402412422432442452462472482492502512522532542552562572582592602612622632642652662672682692702712722732742752762772782792802812822832842852862872882892902912922932942952962972982993003013023033043053063073083093103113123133143153163173183193203213223233243253263273283293303313323333343353363373383393403413423433443453463473483493503513523533543553563573583593603613623633643653663673683693703713723733743753763773783793803813823833843853863873883893903913923933943953963973983994004014024034044054064074084094104114124134144154164174184194204214224234244254264274284294304314324334344354364374384394404414424434444454464474484494504514524534544554564574584594604614624634644654664674684694704714724734744754764774784794804814824834844854864874884894904914924934944954964974984995005015025035045055065075085095105115125135145155165175185195205215225235245255265275285295305315325335345355365375385395405415425435445455465475485495505515525535545555565575585595605615625635645655665675685695705715725735745755765775785795805815825835845855865875885895905915925935945955965975985996006016026036046056066076086096106116126136146156166176186196206216226236246256266276286296306316326336346356366376386396406416426436446456466476486496506516526536546556566576586596606616626636646656666676686696706716726736746756766776786796806816826836846856866876886896906916926936946956966976986997007017027037047057067077087097107117127137147157167177187197207217227237247257267277287297307317327337347357367377387397407417427437447457467477487497507517527537547557567577587597607617627637647657667677687697707717727737747757767777787797807817827837847857867877887897907917927937947957967977987998008018028038048058068078088098108118128138148158168178188198208218228238248258268278288298308318328338348358368378388398408418428438448458468478488498508518528538548558568578588598608618628638648658668678688698708718728738748758768778788798808818828838848858868878888898908918928938948958968978988999009019029039049059069079089099109119129139149159169179189199209219229239249259269279289299309319329339349359369379389399409419429439449459469479489499509519529539549559569579589599609619629639649659669679689699709719729739749759769779789799809819829839849859869879889899909919929939949959969979989991000100110021003100410051006100710081009101010111012101310141015101610171018101910201021102210231024102510261027102810291030103110321033103410351036103710381039104010411042104310441045104610471048104910501051105210531054105510561057105810591060106110621063106410651066106710681069107010711072107310741075107610771078107910801081108210831084108510861087108810891090109110921093109410951096109710981099110011011102110311041105110611071108110911101111111211131114111511161117111811191120112111221123112411251126112711281129113011311132113311341135113611371138113911401141114211431144114511461147114811491150115111521153115411551156115711581159116011611162116311641165116611671168116911701171117211731174117511761177117811791180118111821183118411851186118711881189119011911192119311941195119611971198119912001201120212031204120512061207120812091210121112121213121412151216121712181219122012211222122312241225122612271228122912301231123212331234123512361237123812391240124112421243124412451246124712481249125012511252125312541255125612571258125912601261126212631264126512661267126812691270127112721273127412751276127712781279128012811282128312841285128612871288128912901291129212931294129512961297129812991300130113021303130413051306130713081309131013111312131313141315131613171318131913201321132213231324132513261327132813291330133113321333133413351336133713381339134013411342134313441345134613471348134913501351135213531354135513561357135813591360136113621363136413651366136713681369137013711372137313741375137613771378137913801381138213831384138513861387138813891390139113921393139413951396139713981399140014011402140314041405140614071408140914101411141214131414141514161417141814191420142114221423142414251426142714281429143014311432143314341435143614371438143914401441144214431444144514461447144814491450145114521453145414551456145714581459146014611462146314641465146614671468146914701471147214731474147514761477147814791480148114821483148414851486148714881489149014911492149314941495149614971498149915001501150215031504150515061507150815091510151115121513151415151516151715181519152015211522152315241525152615271528152915301531153215331534153515361537153815391540154115421543154415451546154715481549155015511552155315541555155615571558155915601561156215631564156515661567156815691570157115721573157415751576157715781579158015811582158315841585158615871588158915901591159215931594159515961597159815991600160116021603160416051606160716081609161016111612161316141615161616171618161916201621162216231624162516261627162816291630163116321633163416351636163716381639164016411642164316441645164616471648164916501651165216531654165516561657165816591660166116621663166416651666166716681669167016711672167316741675167616771678167916801681168216831684168516861687168816891690169116921693169416951696169716981699170017011702170317041705170617071708170917101711171217131714171517161717171817191720172117221723172417251726172717281729173017311732173317341735173617371738173917401741174217431744174517461747174817491750175117521753175417551756175717581759176017611762176317641765176617671768176917701771177217731774177517761777177817791780178117821783178417851786178717881789179017911792179317941795179617971798179918001801180218031804180518061807180818091810181118121813181418151816181718181819182018211822182318241825182618271828182918301831183218331834183518361837183818391840184118421843184418451846184718481849185018511852185318541855185618571858185918601861186218631864186518661867186818691870187118721873187418751876187718781879188018811882188318841885188618871888188918901891189218931894189518961897189818991900190119021903190419051906190719081909191019111912191319141915191619171918191919201921192219231924192519261927192819291930193119321933193419351936193719381939194019411942194319441945194619471948194919501951195219531954195519561957195819591960196119621963196419651966196719681969197019711972197319741975197619771978197919801981198219831984198519861987198819891990199119921993199419951996199719981999200020012002200320042005200620072008200920102011201220132014201520162017201820192020202120222023202420252026202720282029203020312032203320342035203620372038203920402041204220432044204520462047204820492050205120522053205420552056205720582059206020612062206320642065206620672068206920702071207220732074207520762077207820792080208120822083208420852086208720882089209020912092209320942095209620972098209921002101210221032104210521062107210821092110211121122113211421152116211721182119212021212122212321242125212621272128212921302131213221332134213521362137213821392140214121422143214421452146214721482149215021512152215321542155215621572158215921602161216221632164216521662167216821692170217121722173217421752176217721782179218021812182218321842185218621872188218921902191219221932194219521962197219821992200220122022203220422052206220722082209221022112212221322142215221622172218221922202221222222232224222522262227222822292230223122322233223422352236223722382239224022412242224322442245224622472248224922502251225222532254225522562257225822592260226122622263226422652266226722682269227022712272227322742275227622772278227922802281228222832284228522862287228822892290229122922293229422952296229722982299230023012302230323042305230623072308230923102311231223132314231523162317231823192320232123222323232423252326232723282329233023312332233323342335233623372338233923402341234223432344234523462347234823492350235123522353235423552356235723582359236023612362236323642365236623672368236923702371237223732374237523762377237823792380238123822383238423852386238723882389239023912392239323942395239623972398239924002401240224032404240524062407240824092410241124122413241424152416241724182419242024212422242324242425242624272428242924302431243224332434243524362437243824392440244124422443244424452446244724482449245024512452245324542455245624572458245924602461246224632464246524662467246824692470247124722473247424752476247724782479248024812482248324842485248624872488248924902491249224932494249524962497249824992500250125022503250425052506250725082509251025112512251325142515251625172518251925202521252225232524252525262527252825292530253125322533253425352536253725382539254025412542254325442545254625472548254925502551255225532554255525562557255825592560256125622563256425652566256725682569257025712572257325742575257625772578257925802581258225832584258525862587258825892590259125922593259425952596259725982599260026012602260326042605260626072608260926102611261226132614261526162617261826192620262126222623262426252626262726282629263026312632263326342635263626372638263926402641264226432644264526462647264826492650265126522653265426552656265726582659266026612662266326642665266626672668266926702671267226732674267526762677267826792680268126822683268426852686268726882689269026912692269326942695269626972698269927002701270227032704270527062707270827092710271127122713271427152716271727182719272027212722272327242725272627272728272927302731273227332734273527362737273827392740274127422743274427452746274727482749275027512752275327542755275627572758275927602761276227632764276527662767276827692770277127722773277427752776277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Thr Phe Ser Ile Gly Leu Ala Val Gly Leu Val Lys Gly Trp Lys Leu  
 130 135 140  
 Thr Leu Val Thr Leu Ser Thr Ser Pro Leu Ile Met Ala Ser Ala Ala  
 145 150 155 160  
 Ala Cys Ser Arg Met Val Ile Ser Leu Thr Ser Lys Glu Leu Ser Ala  
 165 170 175  
 Tyr Ser Lys Ala Gly Ala Val Ala Glu Glu Val Leu Ser Ser Ile Arg  
 180 185 190  
 Thr Val Ile Ala Phe Arg Ala Gln Glu Lys Glu Leu Gln Arg Ser Phe  
 195 200 205  
 Leu Leu Asn Ile Thr Arg Tyr Ala Trp Phe Tyr Phe Pro Gln Trp Leu  
 210 215 220  
 Leu Ser Cys Val Leu Xaa Phe Val Arg Tyr Thr Gln Asn Leu Lys Asp  
 225 230 235 240  
 Ala Lys Asp Phe Gly Ile Lys Arg Thr Ile Ala Ser Lys Val Ser Leu  
 245 250 255  
 Gly Ala Val Tyr Phe Phe Met Asn Gly Thr Tyr Gly Leu Ala Phe Trp  
 260 265 270  
 Tyr Gly Thr Ser Leu Ile Leu Asn Gly Glu Pro Gly Tyr Thr Ile Gly  
 275 280 285  
 Thr Val Leu Ala Val Phe Phe Ser Val Ile His Ser Ser Tyr Cys Ile  
 290 295 300  
 Gly Ala Ala Val Pro His Phe Glu Thr Phe Ala Ile Ala Arg Gly Ala  
 305 310 315 320  
 Ala Phe His Ile Phe Gln Val Ile Asp Lys Lys Pro Ser Ile Asp Asn  
 325 330 335  
 Phe Ser Thr Ala Gly Tyr Lys Pro Glu Ser Ile Glu Gly Thr Val Glu  
 340 345 350  
 Phe Lys Asn Val Ser Phe Asn Tyr Pro Ser Arg Pro Ser Ile Lys Ile  
 355 360 365  
 Leu Lys Gly Leu Asn Leu Arg Ile Lys Ser Gly Glu Thr Val Ala Leu  
 370 375 380  
 Val Gly Leu Asn Gly Ser Gly Lys Ser Thr Val Val Gln Leu Leu Gln  
 385 390 395 400  
 Arg Leu Tyr Asp Pro Asp Asp Gly Phe Ile Met Val Asp Glu Asn Asp  
 405 410 415  
 Ile Arg Ala Leu Asn Val Arg His Tyr Arg Asp His Ile Gly Val Val  
 420 425 430  
 Ser Gln Glu Pro Val Leu Phe Gly Thr Thr Ile Ser Asn Asn Ile Lys  
 435 440 445  
 Tyr Gly Arg Asp Asp Val Thr Asp Glu Glu Met Glu Arg Ala Ala Arg  
 450 455 460

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Glu 465	Ala	Asn	Ala	Tyr	Asp 470	Phe	Ile	Met	Glu	Phe 475	Pro	Asn	Lys	Phe	Asn 480
Thr	Leu	Val	Gly	Glu 485	Lys	Gly	Ala	Gln	Met 490	Ser	Gly	Gly	Gln	Lys 495	Gln
Arg	Ile	Ala	Ile 500	Ala	Arg	Ala	Leu	Val 505	Arg	Asn	Pro	Lys	Ile 510	Leu	Ile
Leu	Asp	Glu 515	Ala	Thr	Ser	Ala	Leu 520	Asp	Ser	Glu	Ser	Lys 525	Ser	Ala	Val
Gln	Ala 530	Ala	Leu	Glu	Lys	Ala 535	Ser	Lys	Gly	Arg	Thr 540	Thr	Ile	Val	Val
Ala 545	His	Arg	Leu	Ser	Thr 550	Ile	Arg	Ser	Ala	Asp 555	Leu	Ile	Val	Thr	Leu 560
Lys	Asp	Gly	Met	Leu 565	Ala	Glu	Lys	Gly	Ala 570	His	Ala	Glu	Leu	Met 575	Ala
Lys	Arg	Gly	Leu 580	Tyr	Tyr	Ser	Leu	Val 585	Met	Ser	Gln	Asp	Ile 590	Lys	Lys
Ala	Asp	Glu 595	Gln	Met	Glu	Ser	Met 600	Thr	Tyr	Ser	Thr	Glu 605	Arg	Lys	Thr
Asn	Ser 610	Leu	Pro	Leu	His	Ser 615	Val	Lys	Ser	Ile	Lys 620	Ser	Asp	Phe	Ile
Asp 625	Lys	Ala	Glu	Glu	Ser 630	Thr	Gln	Ser	Lys	Glu 635	Ile	Ser	Leu	Pro	Glu 640
Val	Ser	Leu	Leu	Lys 645	Ile	Leu	Lys	Leu	Asn 650	Lys	Pro	Glu	Trp	Pro 655	Phe
Val	Val	Leu	Gly 660	Thr	Leu	Ala	Ser	Val 665	Leu	Asn	Gly	Thr	Val 670	His	Pro
Val	Phe 675	Ser	Ile	Ile	Phe	Ala	Lys 680	Ile	Ile	Thr	Met	Phe 685	Gly	Asn	Asn
Asp 690	Lys	Thr	Thr	Leu	Lys	His 695	Asp	Ala	Glu	Ile	Tyr 700	Ser	Met	Ile	Phe
Val 705	Ile	Leu	Gly	Val	Ile 710	Cys	Phe	Val	Ser	Tyr 715	Phe	Met	Gln	Gly	Leu 720
Phe	Tyr	Gly	Arg	Ala 725	Gly	Glu	Ile	Leu	Thr 730	Met	Arg	Leu	Arg	His 735	Leu
Ala	Phe	Lys	Ala 740	Met	Leu	Tyr	Gln	Asp 745	Ile	Ala	Trp	Phe	Asp 750	Glu	Lys
Glu	Asn 755	Ser	Thr	Gly	Gly	Leu	Thr 760	Thr	Ile	Leu	Ala	Ile 765	Asp	Ile	Ala
Gln	Ile 770	Gln	Gly	Ala	Thr	Gly	Ser 775	Arg	Ile	Gly	Val 780	Leu	Thr	Gln	Asn
Ala 785	Thr	Asn	Met	Gly	Leu 790	Ser	Val	Ile	Ile	Ser 795	Phe	Ile	Tyr	Gly	Trp 800

Glu	Met	Thr	Phe	Leu	Ile	Leu	Ser	Ile	Ala	Pro	Val	Leu	Ala	Val	Thr
				805						810				815	
Gly	Met	Ile	Glu	Thr	Ala	Ala	Met	Thr	Gly	Phe	Ala	Asn	Lys	Asp	Lys
			820					825					830		
Gln	Glu	Leu	Lys	His	Ala	Gly	Lys	Ile	Ala	Thr	Glu	Ala	Leu	Glu	Asn
		835					840					845			
Ile	Arg	Thr	Ile	Val	Ser	Leu	Thr	Arg	Glu	Lys	Ala	Phe	Glu	Gln	Met
	850					855					860				
Tyr	Glu	Glu	Met	Leu	Gln	Thr	Gln	His	Arg	Asn	Thr	Ser	Lys	Lys	Ala
865					870					875					880
Gln	Ile	Ile	Gly	Ser	Cys	Tyr	Ala	Phe	Ser	His	Ala	Phe	Ile	Tyr	Phe
				885					890					895	
Ala	Tyr	Ala	Ala	Gly	Phe	Arg	Phe	Gly	Ala	Tyr	Leu	Ile	Gln	Ala	Gly
			900					905					910		
Arg	Met	Thr	Pro	Glu	Gly	Met	Phe	Ile	Val	Phe	Thr	Ala	Ile	Ala	Tyr
		915					920					925			
Gly	Ala	Met	Ala	Ile	Gly	Lys	Thr	Leu	Val	Leu	Ala	Pro	Glu	Tyr	Ser
	930					935					940				
Lys	Ala	Lys	Ser	Gly	Ala	Ala	His	Leu	Phe	Ala	Leu	Leu	Glu	Lys	Lys
945					950					955					960
Pro	Asn	Ile	Asp	Ser	Arg	Ser	Gln	Glu	Gly	Lys	Lys	Pro	Asp	Thr	Cys
				965					970					975	
Glu	Gly	Asn	Leu	Glu	Phe	Arg	Glu	Val	Ser	Phe	Phe	Tyr	Pro	Cys	Arg
			980					985					990		
Pro	Asp	Val	Phe	Ile	Leu	Arg	Gly	Leu	Ser	Leu	Ser	Ile	Glu	Arg	Gly
	995						1000						1005		
Lys	Thr	Val	Ala	Phe	Val	Gly	Ser	Ser	Gly	Cys	Gly	Lys	Ser	Thr	
	1010					1015					1020				
Ser	Val	Gln	Leu	Leu	Gln	Arg	Leu	Tyr	Asp	Pro	Val	Gln	Gly	Gln	
	1025					1030					1035				
Val	Leu	Phe	Asp	Gly	Val	Asp	Ala	Lys	Glu	Leu	Asn	Val	Gln	Trp	
	1040					1045					1050				
Leu	Arg	Ser	Gln	Ile	Ala	Ile	Val	Pro	Gln	Glu	Pro	Val	Leu	Phe	
	1055					1060					1065				
Asn	Cys	Ser	Ile	Ala	Glu	Asn	Ile	Ala	Tyr	Gly	Asp	Asn	Ser	Arg	
	1070					1075					1080				
Val	Val	Pro	Leu	Asp	Glu	Ile	Lys	Glu	Ala	Ala	Asn	Ala	Ala	Asn	
	1085					1090					1095				
Ile	His	Ser	Phe	Ile	Glu	Gly	Leu	Pro	Glu	Lys	Tyr	Asn	Thr	Gln	
	1100					1105					1110				
Val	Gly	Leu	Lys	Gly	Ala	Gln	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	
	1115					1120					1125				

Thr Leu Val Thr Leu Ser Thr Ser Pro Leu Ile Met Ala Ser Ala Ala  
145 150 155 160

Ala	Cys	Ser	Arg	Met 165	Val	Ile	Ser	Leu	Thr 170	Ser	Lys	Glu	Leu	Ser 175	Ala
Tyr	Ser	Lys	Ala 180	Gly	Ala	Val	Ala	Glu 185	Glu	Val	Leu	Ser	Ser 190	Ile	Arg
Thr	Val	Ile 195	Ala	Phe	Arg	Ala	Gln 200	Glu	Lys	Glu	Leu	Gln 205	Arg	Tyr	Thr
Gln	Asn 210	Leu	Lys	Asp	Ala	Lys 215	Asp	Phe	Gly	Ile	Lys 220	Arg	Thr	Ile	Ala
Ser 225	Lys	Val	Ser	Leu 230	Gly	Ala	Val	Tyr	Phe 235	Phe	Met	Asn	Gly	Thr	Tyr 240
Gly	Leu	Ala	Phe	Trp 245	Tyr	Gly	Thr	Ser	Leu 250	Ile	Leu	Asn	Gly	Glu 255	Pro
Gly	Tyr	Thr	Ile 260	Gly	Thr	Val	Leu	Ala 265	Val	Phe	Phe	Ser 270	Val	Ile	His
Ser	Ser	Tyr 275	Cys	Ile	Gly	Ala	Ala 280	Val	Pro	His	Phe 285	Glu	Thr	Phe	Ala
Ile 290	Ala	Arg	Gly	Ala	Ala	Phe 295	His	Ile	Phe	Gln 300	Val	Ile	Asp	Lys	Lys
Pro 305	Ser	Ile	Asp	Asn 310	Phe	Ser	Thr	Ala	Gly	Tyr 315	Lys	Pro	Glu	Ser	Ile 320
Glu	Gly	Thr	Val	Glu 325	Phe	Lys	Asn	Val	Ser 330	Phe	Asn	Tyr	Pro	Ser 335	Arg
Pro	Ser	Ile	Lys 340	Ile	Leu	Lys	Gly	Leu 345	Asn	Leu	Arg	Ile	Lys 350	Ser	Gly
Glu	Thr	Val 355	Ala	Leu	Val	Gly	Leu 360	Asn	Gly	Ser	Gly	Lys 365	Ser	Thr	Val
Val 370	Gln	Leu	Leu	Gln	Arg	Leu 375	Tyr	Asp	Pro	Asp	Asp 380	Gly	Phe	Ile	Met
Val 385	Asp	Glu	Asn	Asp 390	Ile	Arg	Ala	Leu	Asn 395	Val	Arg	His	Tyr	Arg	Asp 400
His	Ile	Gly	Val	Val 405	Ser	Gln	Glu	Pro	Val 410	Leu	Phe	Gly	Thr	Thr 415	Ile
Ser	Asn	Asn 420	Ile	Lys	Tyr	Gly	Arg	Asp 425	Asp	Val	Thr	Asp 430	Glu	Glu	Met
Glu	Arg	Ala 435	Ala	Arg	Glu	Ala	Asn 440	Ala	Tyr	Asp	Phe	Ile 445	Met	Glu	Phe
Pro	Asn 450	Lys	Phe	Asn	Thr	Leu 455	Val	Gly	Glu	Lys	Gly 460	Ala	Gln	Met	Ser
Gly 465	Gly	Gln	Lys	Gln 470	Arg	Ile	Ala	Ile	Ala	Arg 475	Ala	Leu	Val	Arg	Asn 480
Pro	Lys	Ile	Leu	Ile 485	Leu	Asp	Glu	Ala	Thr 490	Ser	Ala	Leu	Asp 495	Ser	Glu

Ser	Lys	Ser	Ala 500	Val	Gln	Ala	Ala	Leu 505	Glu	Lys	Ala	Ser	Lys 510	Gly	Arg
Thr	Thr	Ile 515	Val	Val	Ala	His	Arg 520	Leu	Ser	Thr	Ile	Arg 525	Ser	Ala	Asp
Leu	Ile 530	Val	Thr	Leu	Lys	Asp 535	Gly	Met	Leu	Ala	Glu 540	Lys	Gly	Ala	His
Ala 545	Glu	Leu	Met	Ala	Lys 550	Arg	Gly	Leu	Tyr	Tyr 555	Ser	Leu	Val	Met	Ser 560
Gln	Asp	Ile	Lys	Lys 565	Ala	Asp	Glu	Gln	Met 570	Glu	Ser	Met	Thr	Tyr 575	Ser
Thr	Glu	Arg	Lys 580	Thr	Asn	Ser	Leu	Pro 585	Leu	His	Ser	Val	Lys 590	Ser	Ile
Lys	Ser	Asp 595	Phe	Ile	Asp	Lys	Ala 600	Glu	Glu	Ser	Thr	Gln 605	Ser	Lys	Glu
Ile	Ser 610	Leu	Pro	Glu	Val	Ser 615	Leu	Leu	Lys	Ile	Leu 620	Lys	Leu	Asn	Lys
Pro 625	Glu	Trp	Pro	Phe	Val 630	Val	Leu	Gly	Thr	Leu 635	Ala	Ser	Val	Leu	Asn 640
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Met	Phe	Gly	Asn 660	Asn	Asp	Lys	Thr	Thr 665	Leu	Lys	His	Asp	Ala 670	Glu	Ile
Tyr	Ser	Met 675	Ile	Phe	Val	Ile	Leu 680	Gly	Val	Ile	Cys	Phe 685	Val	Ser	Tyr
Phe 690	Met	Gln	Gly	Leu	Phe	Tyr 695	Gly	Arg	Ala	Gly	Glu 700	Ile	Leu	Thr	Met
Arg 705	Leu	Arg	His	Leu	Ala 710	Phe	Lys	Ala	Met	Leu 715	Tyr	Gln	Asp	Ile	Ala 720
Trp	Phe	Asp	Glu	Lys 725	Glu	Asn	Ser	Thr	Gly 730	Gly	Leu	Thr	Thr	Ile 735	Leu
Ala	Ile	Asp	Ile 740	Ala	Gln	Ile	Gln	Gly 745	Ala	Thr	Gly	Ser	Arg 750	Ile	Gly
Val	Leu	Thr 755	Gln	Asn	Ala	Thr	Asn 760	Met	Gly	Leu	Ser	Val 765	Ile	Ile	Ser
Phe 770	Ile	Tyr	Gly	Trp	Glu	Met 775	Thr	Phe	Leu	Ile	Leu 780	Ser	Ile	Ala	Pro
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Ala	Asn	Lys	Asp	Lys 805	Gln	Glu	Leu	Lys	His 810	Ala	Gly	Lys	Ile	Ala 815	Thr
Glu	Ala	Leu	Glu 820	Asn	Ile	Arg	Thr	Ile 825	Val	Ser	Leu	Thr	Arg 830	Glu	Lys



Ala Phe Glu Gln Met Tyr Glu Glu Met Leu Gln Thr Gln His Arg Asn  
 835 840 845  
 Thr Ser Lys Lys Ala Gln Ile Ile Gly Ser Cys Tyr Ala Phe Ser His  
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 Ala Phe Ile Tyr Phe Ala Tyr Ala Ala Gly Phe Arg Phe Gly Ala Tyr  
 865 870 875 880  
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 Thr Ala Ile Ala Tyr Gly Ala Met Ala Ile Gly Lys Thr Leu Val Leu  
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 Ala Pro Glu Tyr Ser Lys Ala Lys Ser Gly Ala Ala His Leu Phe Ala  
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 Leu Leu Glu Lys Lys Pro Asn Ile Asp Ser Arg Ser Gln Glu Gly Lys  
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 Ser Ile Glu Arg Gly Lys Thr Val Ala Phe Val Gly Ser Ser Gly Cys  
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 Lys Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Gln Lys Pro Lys  
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Asp Leu Ile Val Val Leu His Asn Gly Lys Ile Lys Glu Gln Gly  
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<211> 541

<212> PRT

<213> Homo sapiens

<220>

<221> Note

<222> (230)..(230)

<223> Xaa at position 230 represents any L amino acid

<400> 7

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 Cys Leu Val Gln Thr Asn Thr Tyr Ser Phe Phe Arg Leu Thr Leu Tyr  
 35 40 45  
 Tyr Val Gly Ile Gly Val Ala Ala Leu Ile Phe Gly Tyr Ile Gln Ile  
 50 55 60  
 Ser Leu Trp Ile Ile Thr Ala Ala Arg Gln Thr Lys Arg Ile Arg Lys  
 65 70 75 80  
 Gln Phe Phe His Ser Val Leu Ala Gln Asp Ile Gly Trp Phe Asp Ser  
 85 90 95  
 Cys Asp Ile Gly Glu Leu Asn Thr Arg Met Thr Asp Ile Asp Lys Ile  
 100 105 110  
 Ser Asp Gly Ile Gly Asp Lys Ile Ala Leu Leu Phe Gln Asn Met Ser  
 115 120 125  
 Thr Phe Ser Ile Gly Leu Ala Val Gly Leu Val Lys Gly Trp Lys Leu  
 130 135 140  
 Thr Leu Val Thr Leu Ser Thr Ser Pro Leu Ile Met Ala Ser Ala Ala  
 145 150 155 160  
 Ala Cys Ser Arg Met Val Ile Ser Leu Thr Ser Lys Glu Leu Ser Ala  
 165 170 175

114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

Tyr Ser Lys Ala Gly Ala Val Ala Glu Glu Val Leu Ser Ser Ile Arg  
 180 185 190  
 Thr Val Ile Ala Phe Arg Ala Gln Glu Lys Glu Leu Gln Arg Ser Phe  
 195 200 205  
 Leu Leu Asn Ile Thr Arg Tyr Ala Trp Phe Tyr Phe Pro Gln Trp Leu  
 210 215 220  
 Leu Ser Cys Val Leu Xaa Phe Val Arg Tyr Thr Gln Asn Leu Lys Asp  
 225 230 235 240  
 Ala Lys Asp Phe Gly Ile Lys Arg Thr Ile Ala Ser Lys Val Ser Leu  
 245 250 255  
 Gly Ala Val Tyr Phe Phe Met Asn Gly Thr Tyr Gly Leu Ala Phe Trp  
 260 265 270  
 Tyr Gly Thr Ser Leu Ile Leu Asn Gly Glu Pro Gly Tyr Thr Ile Gly  
 275 280 285  
 Thr Val Leu Ala Val Phe Phe Ser Val Ile His Ser Ser Tyr Cys Ile  
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 Ala Phe His Ile Phe Gln Val Ile Asp Lys Lys Pro Ser Ile Asp Asn  
 325 330 335  
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 Leu Lys Gly Leu Asn Leu Arg Ile Lys Ser Gly Glu Thr Val Ala Leu  
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 Val Gly Leu Asn Gly Ser Gly Lys Ser Thr Val Val Gln Leu Leu Gln  
 385 390 395 400  
 Arg Leu Tyr Asp Pro Asp Asp Gly Phe Ile Met Val Asp Glu Asn Asp  
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 500 505 510

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Ser Lys Val Ser Leu Gly Ala Val Tyr Phe Phe Met Asn Gly Thr Tyr  
225 230 235 240

Gly Leu Ala Phe Trp Tyr Gly Thr Ser Leu Ile Leu Asn Gly Glu Pro  
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 Gly Tyr Thr Ile Gly Thr Val Leu Ala Val Phe Phe Ser Val Ile His  
 260 265 270  
 Ser Ser Tyr Cys Ile Gly Ala Ala Val Pro His Phe Glu Thr Phe Ala  
 275 280 285  
 Ile Ala Arg Gly Ala Ala Phe His Ile Phe Gln Val Ile Asp Lys Lys  
 290 295 300  
 Pro Ser Ile Asp Asn Phe Ser Thr Ala Gly Tyr Lys Pro Glu Ser Ile  
 305 310 315 320  
 Glu Gly Thr Val Glu Phe Lys Asn Val Ser Phe Asn Tyr Pro Ser Arg  
 325 330 335  
 Pro Ser Ile Lys Ile Leu Lys Gly Leu Asn Leu Arg Ile Lys Ser Gly  
 340 345 350  
 Glu Thr Val Ala Leu Val Gly Leu Asn Gly Ser Gly Lys Ser Thr Val  
 355 360 365  
 Val Gln Leu Leu Gln Arg Leu Tyr Asp Pro Asp Asp Gly Phe Ile Met  
 370 375 380  
 Val Asp Glu Asn Asp Ile Arg Ala Leu Asn Val Arg His Tyr Arg Asp  
 385 390 395 400  
 His Ile Gly Val Val Ser Gln Glu Pro Val Leu Phe Gly Thr Thr Ile  
 405 410 415  
 Ser Asn Asn Ile Lys Tyr Gly Arg Asp Asp Val Thr Asp Glu Glu Met  
 420 425 430  
 Glu Arg Ala Ala Arg Glu Ala Asn Ala Tyr Asp Phe Ile Met Glu Phe  
 435 440 445  
 Pro Asn Lys Phe Asn Thr Leu Val Gly Glu Lys Gly Ala Gln Met Ser  
 450 455 460  
 Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Asn  
 465 470 475 480  
 Pro Lys Ile Leu Ile Leu Asp Glu Ala Thr Ser Ala Leu Asp Ser Glu  
 485 490 495  
 Ser Lys Ser Ala Val Gln Ala Ala Leu Glu Lys Asp Thr Pro Arg Tyr  
 500 505 510  
 Ser Phe

&lt;210&gt; 9

&lt;211&gt; 2066

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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 tggcaaaacg aggtctatat tattcacttg tgatgtcaca ggatattaaa aaagctgatg 180  
 aacagatgga gtcaatgaca tattctactg aaagaaagac caactcactt cctctgcact 240  
 ctgtgaagag catcaagtca gacttcattg acaaggctga ggaatccacc caatctaaag 300  
 agataagtct tcctgaagtc tctctattaa aaattttaaa gttaaacaag cctgaatggc 360  
 cttttgtggt tctggggaca ttggcttctg ttctaaatgg aactgttcat ccagtatttt 420  
 ccatcatctt tgcaaaaatt ataaccatgt ttggaaataa tgataaaacc acattaaagc 480  
 atgatgcaga aatttattcc atgatattcg tcattttggg tgttatttgc tttgtcagtt 540  
 atttcatgca gggattattt tacggcagag caggggaaat tttaacgatg agattaagac 600  
 acttggcctt caaagccatg ttatatcagg atattgcctg gtttgatgaa aaggaaaaca 660  
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 tgacaggaat gattgaaacc gcagcaatga ctggatttgc caacaaagat aagcaagaac 900  
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 attttgcta tgcagcaggg ttctgatttg gagcctattt aattcaagct ggacgaatga 1140  
 ccccagaggg catgttcata gtttttactg caattgcata tggagctatg gccatcgga 1200  
 aaacgctcgt tttggctcct gaatattcca aagccaaatc gggggctgcg catctgtttg 1260  
 ccttgttgga aaagaaacca aatatagaca gccgcagtca agaagggaaa aagccagaca 1320  
 catgtgaagg gaatttagag ttctgagaag tctctttctt ctatccatgt cgcccagatg 1380  
 ttttcatcct ccgtggctta tccctcagta ttgagcgagg aaagacagta gcatttgtgg 1440  
 ggagcagcgg ctgtgggaaa agcacttctg ttcaacttct gcagagactt tatgaccccg 1500  
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 gttcccaa at agcaatcggt cctcaagagc ctgtgctctt caactgcagc attgctgaga 1620  
 acatcgcta tggtgacaac agccgtgtgg tgccattaga tgagatcaaa gaagccgcaa 1680  
 atgcagcaaa tatccattct ttattgaag gtctccctga gaaatacaac acacaagttg 1740  
 gactgaaagg agcacagctt tctggcggcc agaaacaaaag actagctatt gcaagggctc 1800  
 ttctccaaaa acccaaaatt ttattgttgg atgaggccac ttcagccctc gataatgaca 1860

gtgagaaggt ggttcagcat gcccttgata aagccaggac gggaaggaca tgcctagtgg 1920  
 tcaactcacag gctctctgca attcagaacg cagatttgat agtggttctg cacaatggaa 1980  
 agataaagga acaaggaact catcaagagc tcctgagaaa tcgagacata tattttaagt 2040  
 tagtgaatgc acagtcagtg cagtga 2066

<210> 10

<211> 2856

<212> DNA

<213> Homo sapiens

<400> 10

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 ttagtgtaat ccatagcagt tattgcattg gagcagcagt ccctcattat tgataagaaa 180  
 ccagtatag ataacttttc cacagctgga tataaacctg aatccataga aggaactgtg 240  
 gaatttaaaa atgtttcttt caattatcca tcaagaccat ctatcaagat tctgaaaggt 300  
 ctgaatctca gaattaagtc tggagagaca gtgcgcttg tgggtctcaa tggcagtggg 360  
 aagagtacgg tagtccagct tctgcagagg ttatatgatc cggatgatgg ctttatcatg 420  
 gtggatgaga atgacatcag agctttaaat gtgcggcatt atcgagacca tattggagtg 480  
 gttagtcaag agcctgtttt gttcgggacc accatcagta acaatatcaa gtatggacga 540  
 gatgatgtga ctgatgaaga gatggagaga gcagcaaggg aagcaaagtc gtatgatttt 600  
 atcatggagt ttctaataa atttaataca ttggtagggg aaaaaggagc tcaaagagt 660  
 ggaggggcaga aacagaggat cgcaattgct cgtgccttag ttcgaaacc caagattctg 720  
 attttagatg aggctacgtc tgccctggat tcagaaagca agtcagctgt tcaagctgca 780  
 ctggagaagg cgagcaaagg tcggactaca atcgtggtag cacaccgact ttctactatt 840  
 cgaagtgcag atttgattgt gaccctaaag gatggaatgc tggcggagaa aggagcacat 900  
 gctgaactaa tggcaaaacg aggtctatat tattcacttg tgatgtcaca ggatattaaa 960  
 aaagctgatg aacagatgga gtcaatgaca tattctactg aaagaaagac caactcatt 1020  
 cctctgcact ctgtgaagag catcaagtca gacttcattg acaaggctga ggaatccacc 1080  
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 cctgaatggc cttttgtggg tctggggaca ttggcttctg ttctaaatgg aactgttcac 1200  
 ccagtatttt ccatcatctt tgcaaaaatt ataaccatgt ttggaaataa tgataaaacc 1260  
 acattaaagc atgatgcaga aatttattcc atgatattcg tcattttggg tgttatttgc 1320

tttgtcagtt atttcatgca gggattattht tacggcagag caggggaaat tttaacgatg 1380  
 agattaagac acttggcctt caaagccatg ttatatcagg atattgcctg gtttgatgaa 1440  
 aaggaaaaca gcacaggagg cttgacaaca atattagcca tagatatagc acaaattcaa 1500  
 ggagcaacag gttccaggat tggcgtctta acacaaaatg caactaacat gggactttca 1560  
 gttatcattt cctttatata tggatgggag atgacattcc tgattctgag tattgctcca 1620  
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 aagcaagaac ttaagcatgc tggaaagata gcaactgaag ctttggagaa tatacgtact 1740  
 atagtgtcat taacaaggga aaaagccttc gagcaaagt atgaagagat gcttcagact 1800  
 caacacagaa atacctcgaa gaaagcacag attattggaa gctgttatgc attcagccat 1860  
 gcctttatat attttgcta tgcagcaggg tttcgatttg gagcctattt aattcaagct 1920  
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 gccatcgaa aaacgctcgt tttggctcct gaatattcca aagccaaatc gggggctgcg 2040  
 catctgtttg ccttgttga aaagaaacca aatatagaca gccgcagtca agaaggga 2100  
 aagccagaca catgtgaagg gaatttagag tttcgagaag tctctttctt ctatccatgt 2160  
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 gataatgaca gtgagaagg ggttcagcat gcccttgata aagccaggac gggaggaca 2700  
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 cacaatggaa agataaagga acaaggaact catcaagagc tcctgagaaa tcgagacata 2820  
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<210> 11

<211> 1175

<212> DNA

<213> Homo sapiens



<400> 11  
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 ttagtgtaat ccatagcagt tattgcattg gagcagcagt ccctcattat tgataagaaa 180  
 cccagtatag ataacttttc cacagctgga tataaacctg aatccataga aggaactgtg 240  
 gaatttaaaa atgttttctt caattatcca tcaagaccat ctatcaagat tctgaaaggt 300  
 ctgaatctca gaattaagtc tggagagaca gtgcgcttgg tcggtctcaa tggcagtggt 360  
 aagagtacgg tagtccagct tctgcagagg ttatatgatc cggatgatgg ctttatcatg 420  
 gtggatgaga atgacatcag agcttttaaat gtgcggcatt atcgagacca tattggagtg 480  
 gttagtcaag agcctgtttt gttcgggacc accatcagta acaatatcaa gtatggacga 540  
 gatgatgtga ctgatgaaga gatggagaga gcagcaaggg aagcaaagtc gtatgatttt 600  
 atcatggagt ttctaataa atttaataca ttggtagggg aaaaaggagc tcaaatgagt 660  
 ggaggggcaga aacagaggat cgcaattgct cgtgccttag ttcgaaaccc caagattctg 720  
 atttttagatg aggctacgtc tgccctggat tcagaaagca agtcagctgt tcaagctgca 780  
 ctggagaagg atacccccag gtattcattt tgacctaat tccactcaag tggagaatcg 840  
 ctgaccttga accagcgccc ttcgacagct ctggccccctc aaacctcacc ctgacctcct 900  
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 ttacactgaa tctaggaggg gagttggcag tggcggtatg aaaaaccatt gaacagtttt 1020  
 ctcgatggcc tgactccctt ataaaccaga gccttcagac cccttacaag gcttaatggc 1080  
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<211> 3177

<212> DNA

<213> Homo sapiens

<220>

<221> Note

<222> (198)..(198)

<223> n at position 198 represents any nucleotide (A, T, C or G)

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 caaagggtctt tcctttttaa tataacaaga tatgcttggt tttattttcc ccagtggcta 180  
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 ggaacctatg gacttgcttt ttggtatgga acctccttga ttcttaatgg agaacctgga 360  
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 gtcggtctca atggcagtg gaagagtacg gtagtccagc ttctgcagag gttatatgat 720  
 ccggatgatg gctttatcat ggtggatgag aatgacatca gagctttaa tgtgcggcat 780  
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<210> 13

<211> 3702

<212> DNA

<213> Homo sapiens

<220>

<221> Note

<222> (723) .. (723)

<223> n at position 723 represents any nucleotide (A, T, C or G)

<400> 13  
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 gttggaatag gtgttgctgc cttgattttt ggttacatac agatttcctt gtggattata 240  
 actgcagcac gacagaccaa gaggattcga aaacagtttt ttcattcagt tttggcacag 300  
 gacatcggct ggtttgatag ctgtgacatc ggtgaactta acactcgcac gacagacatt 360  
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